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[DOCUMENT NAME] SPECIFICATION

[TITLE OF THE INVENTIONS] NOVEL POTASSIUM-DEPENDENT
SODIUM/CALCIUM EXCHANGER

[CLAIMS]

[Claim 1] (1) A polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4, or (2) a polypeptide exhibiting a potassium-dependent sodium-calcium exchange activity and consisting of an amino acid sequence in which 1 to 5 amino acids in total are substituted, deleted, inserted, and/or added at one or plural portions in the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4.

[Claim 2] A polynucleotide encoding the polypeptide according to claim 1.

[Claim 3] An expression vector comprising the polynucleotide according to claim 2.

[Claim 4] A cell transfected with the expression vector according to claim 3.

[Claim 5] A method for producing the polypeptide according to claim 1, characterized by using the cell according to claim 4.

[DETAILED DESCRIPTION OF THE INVENTION]

[0001]

[Technical Field to which the Invention Pertains]

This invention relates to a potassium-dependent sodium-calcium exchanger, which is useful in screening substances useful in treating a cell injury due to postischemic reperfusion.

[0002]

[Prior Art]

During ischemia, an organ proceeds via a reversible to the irreversible phase of cell injury. It is considered that an injury can be avoided if the organ is reperfused in the process, but experimental and clinical examinations point out that the reperfusion per se newly damages the organ. This is called a reperfusion injury. It is known that both free radicals generated during reperfusion and excess intracellular calcium (calcium overload) due to reperfusion play an important role in the generation of reperfusion injuries (Bolli, R. et al., Circulation, 82, p.

723-738, 1990; and Kusuoka, H. et al., Annu. Rev. Physiol., 54, p. 243-256, 1992). Regarding the mechanism of the calcium overload, several hypotheses are proposed, as follows (Kan Kanetsuka, "Kokyu To Junkan", 2001, 49(1), p. 5-11):

(1) Due to a failure of an energy-dependent calcium exchange system, calcium flows into cells in accordance with a concentration gradient thereof.

(2) A concentration of intracellular sodium ions is increased during ischemia, and therefore calcium flows into cells via a sodium-calcium exchange system.

(3) An increased α receptor density during ischemia promotes a calcium overload after reperfusion.

(4) Due to a severe failure of a cell membrane, extracellular calcium flows into cells in accordance with a concentration gradient thereof.

Further, it is considered that, in delayed neuronal cell death during postischemic reperfusion in the brain, a glutamate receptor, NMDA (N-methyl-D-aspartate) receptor, is activated, an NMDA activated calcium channel is opened, and thus calcium flows into cells (Kiichiro Taga, CLINICAL NEUROSCIENCE, 1999, 17(5), p. 567-569).

[0003]

After transient ischemia in an experimental animal, the phenomenon of no reflow (when a blood flow is reflowed, a region where a blood flow is not topically reflowed is generated) is observed in the brain, heart, and kidney. As major mechanisms of the phenomenon of no reflow, hemorrhage and destruction of microvascular construction (for example, capillary embolus by leukocytes, or swelling of vascular endothelial cells), platelet thrombosis, or the like are suggested (Nobuo Araki, "Kokyu To Junkan", 2001, 49(1), p. 13-20). As cells which block microvessels in a focus of middle cerebral artery occlusion, polymorphonuclear leucocytes, monocytes, or platelets are observed in addition to erythrocytes, and particularly, capillary embolus by neutrophils classified into leukocytes is noted as a cause of the phenomenon of no reflow ("Kokyu To Junkan", 2001, 49(1)). When passing through microvessels,

polymorphonuclear leucocytes delay an erythrocyte flow. Further, during ischemia in the brain, polymorphonuclear leucocytes interact with vascular endothelial cells or platelets, and expressions of receptors for adhesion factors are increased at the surfaces of polynuclear leucocytes. Furthermore, monoclonal antibodies against adhesion factors such as L-selection, CD11, CD18, or ICAM-1 attenuated leukocyte accumulation and reduced the area of infarction, and thus it was suggested that the expression of adhesion factors plays an important role in accumulation of leukocytes during postischemic reperfusion (Ma X. L. et al., Circulation, 88, 649-658, 1993; and Yamazaki T. et al., Am. J. Pathol., 143, 410-418, 1993). In addition, it is reported that the expression of adhesion factors in leukocytes is increased by increasing an intracellular calcium concentration (Kooyk Y. et al., Cell Adhes. Commun., 1, 21-32, 1993).

[0004]

There are two types of sodium-calcium exchange reactions, i.e., the classic sodium-calcium exchange reaction and the potassium-dependent sodium-calcium exchange reaction (Tatsu Matsuoka et al., "Tanpakushitsu Kakusan Koso", 1998, 43(12), p. 1555-1560; and Kimura, M., J. Biol. Chem., 268, p.6874-6877, 1993). It is considered that sodium-calcium exchangers exist in all tissues. The physiological function is an extrusion of intracellular calcium outside the cell, accompanied by an influx of extracellular sodium. Further, it is reported that the reverse reaction in which intracellular sodium is extruded and calcium flows into the cell may occur physiologically.

[0005]

[Problems to be Solved by the Invention]

The object of the present invention is to provide a novel potassium-dependent sodium-calcium exchanger, and a novel polynucleotide encoding the polypeptide, and further to provide a convenient screening system for obtaining a substance useful as a therapeutic agent for cell injury due to postischemic reperfusion, of which the therapeutic effect is achieved by inhibiting an activation of leukocytes.

[0006]

[Means for Solving the Problems]

The present invention relates to:

- [1] (1) a polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4, or (2) a polypeptide exhibiting a potassium-dependent sodium-calcium exchange activity and consisting of an amino acid sequence in which 1 to 5 amino acids in total are substituted, deleted, inserted, and/or added at one or plural portions in the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4;
- [2] a polynucleotide encoding the polypeptide of [1];
- [3] an expression vector comprising the polynucleotide of [2];
- [4] a cell transfected with the expression vector of [3];
- and
- [5] a method for producing the polypeptide of [1].

[0007]

[Mode for Carrying out the Invention]

The present invention will be explained in detail hereinafter.

[0008]

1. Polypeptide, polynucleotide, expression vector, and cell of the present invention

The polypeptide of the present invention includes (1) a polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4; and (2) a polypeptide consisting of an amino acid sequence in which 1 to 5 amino acids in total are substituted, deleted, inserted, and/or added at one or plural portions in the amino acid sequence of SEQ ID NO: 2 or 4, and exhibiting a potassium-dependent sodium-calcium exchange activity (hereinafter referred to as a variation functionally equivalent). As the polypeptide of the present invention, the polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4 is preferable.

[0009]

The term "exhibiting a sodium-calcium exchange activity" as used herein means exhibiting an exchange reaction in which intracellular calcium is extruded outside

the cell and extracellular sodium flows into the cell (the forward direction), or exhibiting an exchange reaction in which intracellular sodium is extruded outside the cell and extracellular calcium flows into the cell (the reverse direction). Further, the term "exhibiting a forward sodium-calcium exchange activity" as used herein means exhibiting an exchange reaction in which intracellular calcium is extruded outside the cell and extracellular sodium flows into the cell ($\text{Na}^+_{\text{o}}\text{-Ca}^{2+}_{\text{i}}$ exchange; the forward direction). The term "exhibiting a reverse sodium-calcium exchange activity" as used herein means exhibiting an exchange reaction in which intracellular sodium is extruded outside the cell and extracellular calcium flows into the cell ($\text{Na}^+_{\text{i}}\text{-Ca}^{2+}_{\text{o}}$ exchange; the reverse direction).

[0010]

Whether or not a polypeptide (hereinafter referred to as a test polypeptide) "exhibits a forward sodium-calcium exchange activity", that is, "exhibits an exchange reaction in which intracellular calcium is extruded outside the cell and extracellular sodium flows into the cell (the forward direction)" may be confirmed by a method known to those skilled in the art (Iwamoto T. et al., J. Biol. Chem., 271, 22391-22397, 19962). A method for confirming it is not particularly limited and, for example, the following method may be used.

Cells are transfected with an expression vector comprising a polynucleotide encoding the test polypeptide. The resulting cells are cultured in a medium containing calcium chloride (^{45}Ca chloride) to incorporate calcium ions into the cells; the cells are washed with a washing solution to remove calcium ions not incorporated; the extracellular solution is changed to an extracellular solution for measurement containing sodium ions; and a ^{45}Ca radioactivity contained in the solution is measured. When the radioactivity is detected, it may be confirmed that the test polypeptide "exhibits a forward sodium-calcium exchange activity".

[0011]

Whether or not a test polypeptide "exhibits a reverse

sodium-calcium exchange activity", that is, "exhibits an exchange reaction in which intracellular sodium is extruded outside the cell and extracellular calcium flows into the cell (the reverse direction)" may be confirmed by a method known to those skilled in the art (Iwamoto T. et al., J. Biol. Chem., 271, 22391-22397, 19962). A method for confirming it is not particularly limited and, for example, the following method (preferably a method described in Example 4) may be used.

Cells are transfected with an expression vector comprising a polynucleotide encoding the test polypeptide. The resulting cells are treated with an ionophore (such as monensin) to a univalent cation, to incorporate sodium into the cells; the extracellular solution is changed to a solution containing ^{45}Ca , to exchange intracellular sodium for extracellular calcium; and an intracellular ^{45}Ca radioactivity is measured. When the radioactivity is detected, it may be confirmed that the test polypeptide "exhibits a reverse sodium-calcium exchange activity".

[0012]

Whether or not the sodium-calcium exchange activity of the test compound is "potassium-dependent" may be confirmed by a method known to those skilled in the art (Kimura, M., J. Biol. Chem., 268, p.6874-6877, 1993; Kraev A. et al., J. Biol. Chem., 276, 23161-23172, 2001). A method for confirming it is not particularly limited but, for example, the following method (preferably a method described in Example 4) may be used. More particularly, cells are transfected with an expression vector comprising a polynucleotide encoding the test polypeptide. When measuring the sodium-calcium exchange activity of the resulting cells, a K^+ concentration in the extracellular solution is varied, and an intracellular ^{45}Ca radioactivity in each K^+ concentration is measured. When a higher sodium-calcium exchange activity is detected in the presence of K^+ , it may be confirmed that the sodium-calcium exchange activity of the test compound is "potassium-dependent".

[0013]

The polypeptides consisting of the amino acid sequences

of SEQ ID NOS: 2 and 4, which are included in the polypeptide of the present invention, are novel human potassium-dependent sodium-calcium exchangers consisting of 622 and 603 amino acid residues, respectively. Each polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4 is expressed in peripheral leukocytes, as shown in Example 2.

[0014]

The variation functionally equivalent of the present invention is not particularly limited, so long as it is a polypeptide consisting of an amino acid sequence in which 1 to 5 amino acids, preferably 1 to 3 amino acids, in total are substituted, deleted, inserted, and/or added at one or plural positions (for example, 1 to 3 positions) in the amino acid sequence of SEQ ID NO: 2 or 4, and exhibiting the potassium-dependent sodium-calcium exchange activity. Further, an origin of the variation functionally equivalent is not limited to a human.

[0015]

The variation functionally equivalent of the present invention includes, for example, not only human variations of the polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4, but also variations functionally equivalent derived from organisms other than a human (such as a mouse, a hamster, or a dog). Further, it includes polypeptides prepared using polynucleotides obtained by artificially modifying their amino acid sequences encoded thereby by genetic engineering techniques, on the basis of polynucleotides encoding these native polypeptides (i.e., human variations or variations functionally equivalent derived from organisms other than a human), or on the basis of polynucleotides encoding the amino acid sequence of SEQ ID NO: 2 or 4. The term "variation" as used herein means an individual difference between the same polypeptides in the same species or a difference between homologous polypeptides in several species.

[0016]

The variation functionally equivalent derived from a human or organisms other than a human may be obtained by

those skilled in the art in accordance with the information of the base sequence of SEQ ID NO: 1 or 3 (for example, the sequence consisting of the 14th to 1882nd bases in the base sequence of SEQ ID NO: 1, or the sequence consisting of the 14th to 1825th bases in the base sequence of SEQ ID NO: 3). For example, an appropriate probe or appropriate primers are designed in accordance with the information of the base sequence. A polymerase chain reaction (PCR) method (Saiki, R. K. et al., Science, 239, 487-491, 1988) or a hybridization method is carried out using a sample (for example, total RNA or an mRNA fraction, a cDNA library, or a phage library) prepared from an organism (for example, a mammal such as a human, a mouse, a hamster, or a dog) of interest and the primers or the probe to obtain a polynucleotide encoding the polypeptide. A desired polypeptide may be obtained by expressing the resulting polynucleotide in an appropriate expression system, and then, for example, by confirming that the expressed polypeptide exhibits the sodium-calcium exchange activity by a method described in Example 4, and further confirming that the activity is dependent on a potassium ion by a method described in Example 4. In this connection, genetic engineering techniques may be performed in accordance with known methods (for example, Maniatis, T. et al., "Molecular Cloning-A Laboratory Manual", Cold Spring Harbor Laboratory, NY, 1982), unless otherwise specified.

[0017]

Further, the above artificially-modified polypeptide using a polynucleotide modified artificially by genetic engineering techniques may be obtained by, for example, the following procedure. A polynucleotide encoding the polypeptide is obtained by a conventional method such as site-specific mutagenesis (Mark, D. F. et al., Proc. Natl. Acad. Sci. USA, 81, 5662-5666, 1984). A desired polypeptide may be obtained by expressing the resulting polynucleotide in an appropriate expression system, and then, for example, by confirming that the expressed polypeptide exhibits the sodium-calcium exchange activity by a method described in Example 4, and further confirming that the activity is

dependent on a potassium ion by a method described in Example 4.

[0018]

The polynucleotide of the present invention is not particularly limited, so long as it encodes the polypeptide of the present invention. As the polynucleotide of the present invention, there may be mentioned, for example, a polynucleotide having the sequence consisting of the 14th to 1882nd bases in the base sequence of SEQ ID NO: 1, or the sequence consisting of the 14th to 1825th bases in the base sequence of SEQ ID NO: 3. In this connection, the term "polynucleotide" as used herein includes both DNA and RNA.

[0019]

A method for producing the polynucleotide of the present invention is not particularly limited, but there may be mentioned, for example, (1) a method using PCR, (2) a method using conventional genetic engineering techniques (i.e., a method for selecting a transformant comprising a desired cDNA from strains transformed with a cDNA library), or (3) a chemical synthesis method, as described in WO02/052000. These methods will be explained in this order hereinafter.

[0020]

In the method using PCR, the polynucleotide of the present invention may be produced, for example, by the following procedure.

mRNA is extracted from human cells or tissue capable of producing the polypeptide of the present invention. A pair of primers, between which full-length mRNA corresponding to the polypeptide of the present invention or a partial region of the mRNA is located, is synthesized on the basis of the base sequence of a polynucleotide encoding the polypeptide of the present invention. Full-length cDNA encoding the polypeptide of the present invention or a part of the cDNA may be obtained by performing a reverse transcriptase-polymerase chain reaction (RT-PCR) using the extracted mRNA as a template. Further, a desired DNA fragment may be obtained by digesting the obtained DNA with a restriction enzyme or the like and performing ligation, if desired.

[0021]

In the method using conventional genetic engineering techniques, the polynucleotide of the present invention may be produced, for example, by the following procedure.

First, single-stranded cDNA is synthesized by using reverse transcriptase from mRNA prepared by the above-mentioned PCR method as a template, and then double-stranded cDNA is synthesized from the single-stranded cDNA.

Next, a recombinant plasmid comprising the double-stranded cDNA is prepared and introduced into an Escherichia coli strain, such as DH 5 α , thereby transforming the strain. A transformant is selected using a drug resistance against, for example, tetracycline or ampicillin as a marker. As a method for selecting a transformant containing the cDNA of interest from the resulting transformants, various methods, such as a method for screening a transformant using a synthetic oligonucleotide probe or a method for screening a transformant using a probe produced by PCR, may be used.

A method for collecting the polynucleotide of the present invention from the resulting transformant of interest can be carried out in accordance with a known method (for example, Maniatis, T. et al., "Molecular Cloning-A Laboratory Manual", Cold Spring Harbor Laboratory, NY, 1982). For example, it may be carried out by separating a fraction corresponding to the plasmid DNA from cells and cutting out the cDNA region from the plasmid DNA.

[0022]

In the chemical synthesis method, the polynucleotide of the present invention may be produced, for example, by binding DNA fragments produced by a chemical synthesis method. Each DNA fragment can be synthesized using a DNA synthesizer [for example, Oligo 1000M DNA Synthesizer (Beckman) or 394 DNA/RNA Synthesizer (Applied Biosystems)].

In this connection, codons for each amino acid are known and can be optionally selected and determined by the conventional method, for example, by taking a codon usage of each host to be used into consideration (Crantham, R. et al., Nucleic Acids Res., 9, r43-r74, 1981). Further, a partial modification of codons of these base sequences can

be carried out in accordance with a conventional method, such as site specific mutagenesis using a primer comprised of a synthetic oligonucleotide encoding for a desired modification (Mark, D. F. et al., Proc. Natl. Acad. Sci. USA, 81, 5662-5666, 1984).

[0023]

Determination of the DNA sequences obtained by the above-mentioned methods can be carried out by, for example, a dideoxynucleotide chain termination method (Messing, J. and Vieira, J., Gene, 19, 269-276, 1982). For example, fluorescence labeled dideoxynucleotides are incorporated to a DNA fragment by a PCR method using a reaction solution containing fluorescence labeled dideoxynucleotides. The amplified DNA fragment is electrophoresed in a sequencer (for example, 3700 DNA sequencer; PE Biosystems) and the base sequence thereof can be determined by detecting the fluorescence.

[0024]

The isolated polynucleotide of the present invention is re-integrated into an appropriate vector DNA and a host cell (including a eucaryotic host cell and a procaryotic host cell) may be transformed by the resulting expression vector. Further, it is possible to express the polynucleotide in a desired host cell, by introducing an appropriate promoter and a sequence related to the gene expression into the vector.

[0025]

The expression vector of the present invention is not particularly limited, so long as it comprises the polynucleotide of the present invention. As the expression vector, there may be mentioned, for example, an expression vector obtained by introducing the polynucleotide of the present invention into a known expression vector appropriately selected in accordance with a host cell to be used.

[0026]

The cell of the present invention is not particularly limited, so long as it is transfected with the expression vector of the present invention and comprises the

polynucleotide of the present invention. The cell of the present invention may be, for example, a cell in which the polynucleotide is integrated into a chromosome of a host cell, or a cell containing the polynucleotide as an expression vector comprising the polynucleotide. Further, the cell of the present invention may be a cell expressing the polypeptide of the present invention, or a cell not expressing the polypeptide of the present invention. The cell of the present invention may be obtained by, for example, transfecting a desired host cell with the expression vector of the present invention.

[0027]

In the eucaryotic host cells, for example, cells of vertebrates, insects, and yeast are included. As the vertebral cell, there may be mentioned, for example, a simian COS cell (Gluzman, Y., Cell, 23, 175-182, 1981), a dihydrofolate reductase defective strain of a Chinese hamster ovary cell (CHO-dhfr⁻ cell) (Urlaub, G. and Chasin, L. A., Proc. Natl. Acad. Sci. USA, 77, 4216-4220, 1980), a Chinese hamster lung fibroblast (Dede cell, ATCC: CCL-39) used in Example 4, a human fetal kidney derived HEK293 cell (ATCC: CRL-1573) used in Example 4, a 293-EBNA cell (Invitrogen) obtained by introducing an EBNA-1 gene of Epstein Barr Virus into HEK293 cell, or L929 cell (ATCC: CRL-2148).

[0028]

As an expression vector for a vertebral cell, a vector containing a promoter positioned upstream of the gene to be expressed, an RNA splicing site, a polyadenylation site, a transcription termination sequence, and the like may be generally used. The vector may further contain a replication origin, if necessary. As the expression vector, there may be mentioned, for example, pSV2dhfr containing an SV40 early promoter (Subramani, S. et al., Mol. Cell. Biol., 1, 854-864, 1981), pEF-BOS containing a human elongation factor promoter (Mizushima, S. and Nagata, S., Nucleic Acids Res., 18, 5322, 1990), pCEP4 containing a cytomegalovirus promoter (Invitrogen), pIRESneo2 (CLONTECH), or pCDNA3.1 (Invitrogen).

[0029]

When the COS cell is used as the host cell, a vector which has an SV40 replication origin, can perform an autonomous replication in the COS cell, and has a transcription promoter, a transcription termination signal, and an RNA splicing site, may be used as the expression vector. As the vector, there may be mentioned, for example, pME18S (Maruyama, K. and Takebe, Y., Med. Immunol., 20, 27-32, 1990), pEF-BOS (Mizushima, S. and Nagata, S., Nucleic Acids Res., 18, 5322, 1990), or pCDM8 (Seed, B., Nature, 329, 840-842, 1987).

[0030]

The expression vector may be incorporated into COS cells by, for example, a DEAE-dextran method (Luthman, H. and Magnusson, G., Nucleic Acids Res., 11, 1295-1308, 1983), a calcium phosphate-DNA co-precipitation method (Graham, F. L. and van der Ed, A. J., Virology, 52, 456-457, 1973), a method using a commercially available transfection reagent (for example, FuGENETM6 Transfection Reagent; Roche Diagnostics), or an electroporation method (Neumann, E. et al., EMBO J., 1, 841-845, 1982).

[0031]

When the CHO cell is used as the host cell, a transformant capable of stably producing the polypeptide of the present invention can be obtained by carrying out a co-transfection of an expression vector comprising the polynucleotide of the present invention, together with a vector capable of expressing a neo gene which functions as a G418 resistance marker, such as pRSVneo (Sambrook, J. et al., "Molecular Cloning-A Laboratory Manual", Cold Spring Harbor Laboratory, NY, 1989) or pSV2-neo (Southern, P. J. and Berg, P., J. Mol. Appl. Genet., 1, 327-341, 1982), and selecting a G418 resistant colony.

[0032]

When the 293-EBNA cell is used as the host cell, for example, pCEP4 (Invitrogen) containing a replication origin of Epstein Barr Virus and capable of performing an autonomous replication in the 293-EBNA cell may be used as the expression vector.

[0033]

The cell of the present invention may be cultured in accordance with the conventional method, and the polypeptide of the present invention is produced at the surface of the cell. As a medium to be used in the culturing, a medium commonly used in a desired host cell may be appropriately selected. In the case of the COS cell or Dede cell, for example, a medium such as an RPMI-1640 medium or a Dulbecco's modified Eagle's minimum essential medium (DMEM) may be used, by supplementing it with a serum component such as fetal bovine serum (FBS) if necessary. In the case of the 293-EBNA cell, a medium such as a Dulbecco's modified Eagle's minimum essential medium (DMEM) with a serum component such as fetal bovine serum (FBS) and G418 may be used.

[0034]

The polypeptide of the present invention produced at the cell surface by culturing the cell of the present invention may be separated and purified therefrom by various known separation techniques making use of the physical properties, chemical properties and the like of the polypeptide. More particularly, a cell membrane fraction containing the polypeptide of the present invention may be obtained by culturing cells expressing the polypeptide of the present invention, suspending them in a buffer, homogenizing them, and centrifuging the resulting homogenate. After the obtained cell membrane fraction was solubilized, the polypeptide of the present invention may be purified by a commonly used treatment, for example, a treatment with a protein precipitant, ultrafiltration, various liquid chromatography techniques such as molecular sieve chromatography (gel filtration), adsorption chromatography, ion exchange chromatography, affinity chromatography, or high performance liquid chromatography (HPLC), or dialysis, or a combination thereof.

[0035]

2. Screening of therapeutic agents for cell injury due to postischemic reperfusion

A substance which inhibits the polypeptide of the

present invention can be screened by using the cell expressing the polypeptide of the present invention so as to exhibit the potassium-dependent sodium-calcium exchange activity.

As described in BACKGROUND ART, it is known that the intracellular calcium overload due to reperfusion plays an important role in the generation of a reperfusion injury and that the potassium-dependent sodium-calcium exchanger is involved in the calcium influx into the cell accompanied by the extrusion of intracellular sodium (reverse direction). Further, it is known that the sodium-calcium exchanger extrudes intracellular sodium outside the cell and incorporates calcium into the cell during postischemic reperfusion, to return the intracellular sodium overload caused by reperfusion to the original state. Furthermore, it is known that an expression of adhesive factors in leukocytes was increased by an increased intracellular calcium concentration, and that monoclonal antibodies against the adhesive factors suppressed the leukocyte accumulation and reduced the area of infarction. Therefore, it is considered that an inhibition of an intracellular calcium overload in leukocytes suppresses the leukocyte accumulation and leukocyte activation by adhesive factors due to the overload, and has an activity of avoiding cell injury caused by the phenomenon of no reflow.

The polypeptide of the present invention consisting of the sequence of SEQ ID NO: 2 or 4 is a potassium-dependent sodium-calcium exchanger expressed abundantly in peripheral leukocytes. Therefore, it is considered that an agent inhibiting or suppressing the potassium-dependent sodium-calcium exchange (reverse direction) in the polypeptide of the present invention suppresses calcium influx into the cell and inhibits the leukocyte activation or adhesion, and thus is useful in the treatment of a cell injury due to postischemic reperfusion.

[0036]

Therefore, the cell of the present invention per se may be used as a screening tool for a therapeutic agent for cell injury due to postischemic reperfusion (particularly an

inhibitor of the polypeptide of the present invention).

The term "inhibiting or suppressing the polypeptide of the present invention" means inhibiting or suppressing the potassium-dependent sodium-calcium exchange activity, including the case of inhibiting or suppressing the potassium-dependent sodium-calcium exchange activity by inhibiting or suppressing the expression of the polypeptide.

[0037]

The method for screening a therapeutic agent for cell injury due to postischemic reperfusion (particularly an inhibitor of the polypeptide of the present invention) comprises the steps of:
bringing the cell of the present invention into contact with a compound to be tested, and
analyzing whether or not the polypeptide is inhibited.

[0038]

Compounds to be tested which may be applied to the screening method of the present invention are not particularly limited, but there may be mentioned, for example, various known compounds (including peptides) registered in chemical files, compounds obtained by combinatorial chemistry techniques (Terrett, N. K. et al., Tetrahedron, 51, 8135-8137, 1995), or random peptides prepared by employing a phage display method (Felici, F. et al., J. Mol. Biol., 222, 301-310, 1991) or the like. In addition, culture supernatants of microorganisms, natural components derived from plants or marine organisms, or animal tissue extracts may be used as the test compounds for screening. Further, compounds (including peptides) obtained by chemically or biologically modifying compounds (including peptides) selected by the screening method of the present invention may be used.

[0039]

The screening method of the present invention is not particularly limited, so long as it comprises the steps of:
bringing a cell expressing the polypeptide of the present invention so as to function as the potassium-dependent sodium-calcium exchanger (i.e., including a cell which was transfected with an expression vector comprising a

polynucleotide encoding the polypeptide of the present invention and expresses the polypeptide so as to function as the potassium-dependent sodium-calcium exchanger, and a naturally occurring cell which expresses the polypeptide of the present invention so as to function as the potassium-dependent sodium-calcium exchanger) into contact with a compound to be tested, and

(2) analyzing whether or not the polypeptide is inhibited. There may be mentioned, on the basis of differences in methods used for analyzing the inhibition of the polypeptide of the present invention, for example,

[1] a screening method utilizing a radioisotope $^{45}\text{Ca}^{2+}$ ion uptake, or

[2] a screening method utilizing a calcium sensitive dye.

Among these methods, the screening method utilizing a radioisotope $^{45}\text{Ca}^{2+}$ ion uptake is preferable. As the cell used in the screening, the cell of the present invention prepared by transfecting it with an expression vector comprising a polynucleotide encoding the polypeptide of the present invention is preferable.

[0040]

According to the above method [1], a substance which inhibits the polypeptide of the present invention and is useful in treating cell injury due to postischemic reperfusion may be screened by the following method. Sodium is incorporated into cells expressing the polypeptide of the present invention at the cell surface, using an ionophore (such as monensin) to a univalent cation; the extracellular solution is changed to a radioisotope $^{45}\text{Ca}^{2+}$ ion-containing extracellular solution with or without a test compound; and an intracellular $^{45}\text{Ca}^{2+}$ radioactivity is measured. Then, whether or not the polypeptide of the present invention is inhibited is analyzed, on the basis of the difference in amounts of radioactivity incorporated into cells in the presence or absence of the test compound. That is, the screening method [1] of the present invention comprises the steps of:

incorporating radioisotope $^{45}\text{Ca}^{2+}$ ions into the cell expressing the polypeptide of the present invention at the

cell surface, and simultaneously, bringing the cell into contact with a compound to be tested, and detecting an amount of radioactivity incorporated into the cell.

[0041]

For example, the cells expressing the polypeptide of the present invention are treated with an extracellular solution containing a test compound and monensin, to incorporate sodium into the cells. The extracellular solution is changed to an extracellular solution containing the test compound and $^{45}\text{Ca}^{2+}$, to incorporate $^{45}\text{Ca}^{2+}$ into the cells by the sodium-calcium exchange activity. The cells are washed with a solution containing lanthanum, an inhibitor of the sodium-calcium exchange activity, to remove $^{45}\text{Ca}^{2+}$ not incorporated. When the reverse sodium-calcium exchange activity is inhibited, an amount of $^{45}\text{Ca}^{2+}$ influx into the cells is decreased, and thus whether or not the polypeptide of the present invention is inhibited can be analyzed on the basis of the radioactivity in the cells as an indicator of the reverse sodium-calcium exchange activity. More particularly, it is preferable to detect the reverse sodium-calcium exchange activity by the method described in Example 4. An inhibitor of the polypeptide of the present invention can be screened by analyzing a change of radioactivity incorporated into the cells by adding the test compound.

[0042]

When screening a substance which inhibits the polypeptide of the present invention and is useful in treating a cell injury due to postischemic reperfusion, by the above method [2], a calcium sensitive dye is incorporated into the cells expressing the polypeptide of the present invention at the cell surface, and then whether or not the polypeptide of the present invention is inhibited is analyzed, on the basis of a change of a fluorescence intensity thereof in the cells in the presence or absence of the test compound. That is, in the screening method [2] of the present invention, the cells expressing the polypeptide of the present invention at the cell surface are treated

with an extracellular solution containing an ionophore (such as monensin) to a univalent cation, to incorporate sodium into the cells. The extracellular solution is changed to an extracellular solution containing a test compound and a calcium sensitive dye, to incorporate the calcium sensitive dye into the cells by the sodium-calcium exchange activity. The cells are washed with a solution containing an inhibitor of the sodium-calcium exchange activity such as lanthanum, to remove the calcium sensitive dye not incorporated. When the reverse sodium-calcium exchange activity is inhibited, a fluorescence intensity of the calcium sensitive dye in the cells is decreased, and thus whether or not the polypeptide of the present invention is inhibited can be analyzed, on the basis of the fluorescence intensity in the cells as an indicator of the reverse sodium-calcium exchange activity. An inhibitor of the polypeptide of the present invention can be screened by detecting the fluorescence intensity of the calcium sensitive dye in the presence of the test compound. The screening method comprises the steps of: incorporating a calcium sensitive dye into the cell, and then bringing the cell into contact with a compound to be tested, and detecting the fluorescence intensity of the calcium sensitive dye in the cell. This screening utilizes the feature that a calcium sensitive dye can optically detect calcium influx accompanied by the reverse-mode activation of sodium-calcium exchanger.

[0043]

More particularly, the activity of the polypeptide of the present invention can be detected using, for example, Fura-2 or a derivative thereof as the calcium sensitive dye. An inhibitor of the polypeptide of the present invention can be screened by comparing a change of the fluorescence intensity of the dye in the presence or absence of the test compound. When the reverse sodium-calcium exchange activity is inhibited, the fluorescence intensity is decreased.

[0044]

[EXAMPLES]

The present invention now will be further illustrated

by, but is by no means limited to, the following Examples. The procedures were performed in accordance with the known methods (for example, Maniatis, T., et al., "Molecular Cloning - A Laboratory Manual", Cold Spring Harbor Laboratory, NY, 1982; and Hille, B., Ionic Channels of Excitable Membranes, 2nd Ed., Sinauer Associates Inc., MA, 1992), unless otherwise specified.

[0045]

Example 1: Isolation of genes encoding novel potassium-dependent sodium-calcium exchangers and construction of expression vectors

A full-length cDNA encoding each novel sodium-calcium exchanger of the present invention having the amino acid sequence of SEQ ID NO: 2 or 4 was obtained by a reverse transcriptase-polymerase chain reaction (RT-PCR) method using human brain cDNA (Marathon-Ready cDNA; Clontech) as a template, by the following procedure.

[0046]

A PCR was carried out using human brain cDNA (Marathon-Ready cDNA; Clontech) as a template, an oligonucleotide consisting of the base sequence of SEQ ID NO: 5 (having the EcoRI recognition sequence added to the 5'-terminus) as a forward primer, an oligonucleotide consisting of the base sequence of SEQ ID NO: 6 (having the KpnI recognition sequence added to the 5'-terminus) as a reverse primer, and DNA Polymerase (PLATINUM Taq DNA Polymerase High-Fidelity; GIBCO-BRL). In the PCR, a thermal denaturation was first performed at 95°C for 1 minute, and then a cycle consisting of reactions at 98°C for 10 seconds, at 60°C for 20 seconds, and at 72°C for 3 minutes was repeated 40 times. As a result, two DNA bands of approximately 1.9 kbp were amplified. The longer DNA fragment was designated "622" and the shorter one was designated "603".

[0047]

Each DNA fragment was digested with restriction enzymes EcoRI and KpnI, and cloned into plasmid pcDNA3.1 (Invitrogen). The resulting clones were designated pcDNA-622 and pcDNA-603. In this connection, the plasmid pcDNA3.1 contains a cytomegalovirus promoter sequence and may be used

for expressing a novel potassium-dependent sodium-calcium exchanger in an animal cell.

[0048]

The base sequences of the clones pcDNA-622 and pcDNA-603 were analyzed using a DNA sequencer (ABI377 DNA Sequencer; Applied Biosystems) by a dideoxy terminator method to obtain the base sequences of SEQ ID NOS: 1 and 3, respectively.

The base sequence of SEQ ID NO: 1 (total base pairs = 1902 bp) contains an open reading frame represented by the sequence consisting of the 14th to 1882nd bases. The amino acid sequence deduced from the open reading frame and consisting of 622 amino acid residues was that of SEQ ID NO: 2.

The base sequence of SEQ ID NO: 3 (total base pairs = 1845 bp) contains an open reading frame represented by the sequence consisting of the 14th to 1825th bases. The amino acid sequence deduced from the open reading frame and consisting of 603 amino acid residues was that of SEQ ID NO: 4.

[0049]

Example 2: Analysis of expression distribution of potassium-dependent sodium-calcium exchangers in human tissues

An expression distribution of the gene (SEQ ID NO: 1) encoding the novel potassium-dependent sodium-calcium in human tissues was analyzed by a reverse transcriptase-polymerase chain reaction (RT-PCR) method in accordance with the following procedure.

Poly A⁺ RNA (5 ng, respectively; Clontech) from each human tissue was treated with DNase, and then a first-strand cDNA was synthesized by carrying out a reverse transcription using an RT-PCR kit (SUPERScript First-Strand Synthesis System for RT-PCR; GIBCO-BRL).

A PCR was carried out using the resulting first-strand cDNA as a template, an oligonucleotide consisting of the base sequence of SEQ ID NO: 7 as a forward primer, an oligonucleotide consisting of the base sequence of SEQ ID NO: 8 as a reverse primer, and DNA Polymerase (PLATINUM Taq DNA Polymerase High-Fidelity; GIBCO-BRL). In the PCR, a

thermal denaturation was first performed at 94°C for 1 minute, and then a cycle consisting of reactions at 98°C for 10 seconds, at 64°C for 20 seconds, and at 68°C for 1 minute and 30 seconds was repeated 35 times. In this connection, the base sequences of the primers are specific sequences commonly contained in both genes encoding the polypeptides consisting of the amino acid sequences of SEQ ID NOS: 2 and 4.

[0050]

When the RT-PCR analysis of human peripheral leukocytes was carried out, DNA fragments of approximately 750 bp and approximately 700 bp were amplified. The DNA fragments of approximately 750 bp and approximately 700 bp contained "the sequence consisting of the 348th to 1101st bases in the base sequence of SEQ ID NO: 1" and "the sequence consisting of the 348th to 1044th bases in the base sequence of SEQ ID NO: 3", respectively. From the result, it was found that the mRNA of each potassium-dependent sodium-calcium exchanger of the present invention was expressed in human peripheral leukocytes.

[0051]

Example 3: Expression of potassium-dependent sodium-calcium exchangers in animal cells HEK293, CCL-39, and CHO

Each polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4 was expressed in animal cells to detect a novel potassium-dependent sodium-calcium exchange activity of the polypeptide. As the animal cells, an HEK293 cell (ATCC: CRL-1573), a Dede cell (ATCC: CCL-39), and a CHO-dhfr⁻ cell (ATCC: CRL-9096) were used. HEK293 cells, Dede cells, or CHO-dhfr⁻ cells were transfected with the expression vector pCDNA-622 or pCDNA-603 prepared in Example 1 and a commercially available transfection reagent (LipofectAMINE2000; GIBCO-BRL) to express each potassium-dependent sodium-calcium exchanger in each cell. In this connection, the concrete procedure was carried out in accordance with a manual attached to the transfection reagent. Further, a cell transfected with the plasmid pCDNA3.1 was prepared as a control cell in a similar fashion. The resulting transfected cells were used in the following

Example 4.

[0052]

Example 4: Detection of potassium-dependent sodium-calcium exchange activity

The sodium-calcium exchange activity was measured using each of the cells prepared in Example 3.

Sodium was incorporated into cells by changing the medium to an extracellular solution containing monensin [i.e., a solution containing 0.01 mmol/L monensin, 1 mmol/L ouabain, 146 mmol/L NaCl, 4 mmol/L KCl, 0.1 mmol/L CaCl₂, 2 mmol/L MgCl₂, 10 mmol/L glucose, 0.1% bovine serum albumin, and 10 mmol/L HEPES-Tris (pH=7.4)] and incubating the cells at 37°C for 30 minutes. The solution was changed to an extracellular solution containing calcium chloride (⁴⁵CaCl₂; 55.5 kBq/mL) [i.e., a solution containing 0.01 mmol/L verapamil, 1 mmol/L ouabain, 150 mmol/L NaCl, 0.1 mmol/L CaCl₂, 2 mmol/L MgCl₂, 10 mmol/L glucose, 0.1% bovine serum albumin, and 10 mmol/L HEPES-Tris (pH=7.4); extracellular solution A], and the cells were allowed to stand at room temperature for 15 minutes to exchange the intracellular sodium ions for the calcium ions.

In addition, an extracellular solution in which choline chloride was substituted for NaCl was used. Further, to examine the dependency on a potassium ion, an extracellular solution containing calcium chloride (⁴⁵CaCl₂; 55.5 kBq/mL) and potassium chloride [i.e., a solution containing 0.01 mmol/L verapamil, 1 mmol/L ouabain, 4 mmol/L KCl, 146 mmol/L choline chloride, 0.1 mmol/L CaCl₂, 2 mmol/L MgCl₂, 10 mmol/L glucose, 0.1% bovine serum albumin, and 10 mmol/L HEPES-Tris (pH=7.4)] was used.

[0053]

The treated cells were washed with a washing solution containing 120 mmol/L choline chloride, 10 mmol/L LaCl₃, and 10 mmol/L HEPES-Tris (pH=7.4) to remove calcium ions not incorporated, and then an intracellular calcium ion radioactivity was measured and analyzed by a liquid scintillation counter. In the HEK293 cells, Dede cells, or CHO-dhfr⁻ cells expressing the polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4, a higher

radioactivity was measured when using the extracellular solution in which sodium was replaced with choline. Further, higher radioactivity was measured when using the extracellular solution containing potassium.

[0054]

As described above, it was confirmed that, in the cells expressing the polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 or 4 of the present invention, intracellular sodium ions can be exchanged for extracellular calcium ions more effectively in the presence of potassium ions, and that the polypeptide of the present invention consisting of the amino acid sequence of SEQ ID NO: 2 or 4 exhibits a potassium-dependent sodium-calcium exchange activity.

[0055]

[Effects of the Invention]

The polypeptide of the present invention is a potassium-dependent sodium-calcium exchanger expressed in peripheral leukocytes, and thus promotes cell injury due to postischemic reperfusion. Therefore, a substance which inhibits the polypeptide of the present invention is useful in treating cell injury due to postischemic reperfusion.

Further, the polypeptide of the present invention and the cell of the present invention expressing the polypeptide at the surface thereof are useful in screening a therapeutic agent for cell injury due to postischemic reperfusion. A convenient screening system for obtaining a therapeutic agent for cell injury due to postischemic reperfusion can be provided by using the cell of the present invention. Furthermore, the polynucleotide and the expression vector of the present invention is useful in manufacturing a screening tool for a therapeutic agent for cell injury.

[0056]

[Free Text in Sequence Listing]

Features of "Artificial Sequence" are described in the numeric identifier <223> in the Sequence Listing. More particularly, each of the base sequences of SEQ ID NOS: 5 to 8 is an artificially synthesized primer sequence.

[0057]

[Sequence Listing]

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<120> Novel potassium-dependent sodium/calcium exchanger

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<160> 8

<170> PatentIn version 3.1

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<223>

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	1				5					10				

cgc	agg	agg	cga	gag	atg	ctg	ccg	cag	caa	gtc	ggc	ttc	gtg	tgc	gcg	97
Arg	Arg	Arg	Arg	Glu	Met	Leu	Pro	Gln	Gln	Val	Gly	Phe	Val	Cys	Ala	
	15					20					25					

gtg	ctg	gcc	ctg	gtg	tgc	tgt	gcg	tcc	ggc	ctc	ttc	ggc	agc	ttg	ggg	145
Val	Leu	Ala	Leu	Val	Cys	Cys	Ala	Ser	Gly	Leu	Phe	Gly	Ser	Leu	Gly	
	30					35					40					

cac	aaa	aca	gct	tct	gct	agc	aaa	cgt	gtc	ctg	cca	gac	aca	tgg	aga	193
His	Lys	Thr	Ala	Ser	Ala	Ser	Lys	Arg	Val	Leu	Pro	Asp	Thr	Trp	Arg	
45					50				55					60		

aat	aga	aag	ttg	atg	gcc	cca	gtg	aat	ggg	aca	cag	aca	gcc	aag	aac	241
Asn	Arg	Lys	Leu	Met	Ala	Pro	Val	Asn	Gly	Thr	Gln	Thr	Ala	Lys	Asn	
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tgc	aca	gat	cct	gcg	att	cac	gag	ttc	ccc	aca	gat	ctg	ttc	tcc	aat	289
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Cys	Thr	Asp	Pro	Ala	Ile	His	Glu	Phe	Pro	Thr	Asp	Leu	Phe	Ser	Asn	
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Gly	Leu	Phe	Ala	Gly	Gln	Val	Val	Arg	Leu	Thr	Trp	Trp	Ala	Val	Cys	
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cga	gac	tcc	gtg	tac	tac	acc	atc	tct	gtc	atc	gtg	ctc	atc	gtg	ttc	673
Arg	Asp	Ser	Val	Tyr	Tyr	Thr	Ile	Ser	Val	Ile	Val	Leu	Ile	Val	Phe	
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Asn Ser Glu Leu Glu Ala Gly Asn Asp Phe Tyr Asp Gly Ser Tyr Asp			
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Asp Pro Ser Val Pro Leu Leu Gly Gln Val Lys Glu Lys Pro Gln Tyr			
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ccc aag ttc acc ttc cct gaa gca ggc tta cga atc atg atc acc aat			1009
Pro Lys Phe Thr Phe Pro Glu Ala Gly Leu Arg Ile Met Ile Thr Asn			
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aag ttt gga ccc agg acc cga cta cgg atg gcc agc agg atc atc att			1057
Lys Phe Gly Pro Arg Thr Arg Leu Arg Met Ala Ser Arg Ile Ile Ile			
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Pro Leu Gln Asn Gly Arg His Glu Asn Ile Glu Asn Gly Asn Val Pro			
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Ser Pro Phe Ser Val Pro Glu Ala Arg Gly Asp Lys Val Lys Trp Val			
415	420	425	
ttc acc tgg ccc ctc atc ttc ctc ctg tgc gtc acc att ccc aac tgc			1345
Phe Thr Trp Pro Leu Ile Phe Leu Leu Cys Val Thr Ile Pro Asn Cys			
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1902

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	195	200 205
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Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile Leu Tyr Val Phe		
	225	230 235 240
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Pro Leu Leu Gly Gln Val Lys Glu Lys Pro Gln Tyr Gly Lys Asn Pro		
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Val Val Met Val Asp Glu Ile Met Ser Ser Ser Pro Pro Lys Phe Thr		
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Ser Leu Glu Lys Ile Cys Glu Arg Leu His Leu Ser Glu Asp Val Ala	
125 130 135 140	
gga gcc acc ttc atg gct gca gga agc tca acg cca gag ctg ttt gcg	481
Gly Ala Thr Phe Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala	
145 150 155	
tct gtt att ggg gtg ttc atc acc cac ggg gac gtc ggg gtg ggc acc	529
Ser Val Ile Gly Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr	
160 165 170	
atc gtg ggc tct gct gtg ttc aac atc ctg tgc ata att gga gtg tgc	577

Ile Val Gly Ser Ala Val Phe Asn Ile Leu Cys Ile Ile Gly Val Cys	
175 180 185	
gga ctg ttt gct ggc cag gtg gtc cgt ctg acg tgg tgg gcc gtg tgc	625
Gly Leu Phe Ala Gly Gln Val Val Arg Leu Thr Trp Trp Ala Val Cys	
190 195 200	
cga gac tcc gtg tac tac acc atc tot gtc atc gtg ctc atc gtg ttc	673
Arg Asp Ser Val Tyr Tyr Thr Ile Ser Val Ile Val Leu Ile Val Phe	
205 210 215 220	
ata tat gat gaa caa att gtg tgg tgg gaa ggc ctg gtg ctc atc atc	721
Ile Tyr Asp Glu Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile	
225 230 235	
ttg tat gtg ttt tat att ctg atc atg aag tac aat gtg aag atg caa	769
Leu Tyr Val Phe Tyr Ile Leu Ile Met Lys Tyr Asn Val Lys Met Gln	
240 245 250	
gcc ttt ttc aca gtc aaa caa aag agc att gca aac ggt aac ccg gtc	817
Ala Phe Phe Thr Val Lys Gln Lys Ser Ile Ala Asn Gly Asn Pro Val	
255 260 265	
aac agt gag ctg gag gct gtg aag gag aag cca cag tat ggc aag aac	865
Asn Ser Glu Leu Glu Ala Val Lys Glu Lys Pro Gln Tyr Gly Lys Asn	
270 275 280	
ccc gtg gtg atg gtg gac gag att atg agc tcc agc cct ccc aag ttc	913
Pro Val Val Met Val Asp Glu Ile Met Ser Ser Ser Pro Pro Lys Phe	
285 290 295 300	
acc ttc cct gaa gca ggc tta cga atc atg atc acc aat aag ttt gga	961
Thr Phe Pro Glu Ala Gly Leu Arg Ile Met Ile Thr Asn Lys Phe Gly	
305 310 315	
ccc agg acc cga cta cgg atg gcc agc agg atc atc att aat gag cgg	1009
Pro Arg Thr Arg Leu Arg Met Ala Ser Arg Ile Ile Ile Asn Glu Arg	
320 325 330	
cag aga ctg atc aac tcg gcc aat ggt gtg agc agt aag ccg ctt caa	1057
Gln Arg Leu Ile Asn Ser Ala Asn Gly Val Ser Ser Lys Pro Leu Gln	
335 340 345	
aac ggg agg cac gag aac att gag aac ggg aat gtt cct gtg gaa aac	1105
Asn Gly Arg His Glu Asn Ile Glu Asn Gly Asn Val Pro Val Glu Asn	

350	355	360	
ccc gaa gac cct cag cag aat cag gag cag cag ccg ccg cca cag cca			1153
Pro Glu Asp Pro Gln Gln Asn Gln Glu Gln Gln Pro Pro Pro Gln Pro			
365	370	375	380
cca ccg cca gag cca gag ccg gtg gag gct gac ttc ctg tcc ccc ttc			1201
Pro Pro Pro Glu Pro Glu Pro Val Glu Ala Asp Phe Leu Ser Pro Phe			
385	390		395
tcc gtg ccg gag gcc aga ggg gac aag gtc aag tgg gtg ttc acc tgg			1249
Ser Val Pro Glu Ala Arg Gly Asp Lys Val Lys Trp Val Phe Thr Trp			
400	405		410
ccc ctc atc ttc ctc ctg tgc gtc acc att ccc aac tgc agc aag ccc			1297
Pro Leu Ile Phe Leu Leu Cys Val Thr Ile Pro Asn Cys Ser Lys Pro			
415	420		425
cgc tgg gag aag ttc ttc atg gtc acc ttc atc acc gcc acg ctg tgg			1345
Arg Trp Glu Lys Phe Phe Met Val Thr Phe Ile Thr Ala Thr Leu Trp			
430	435		440
atc gct gtg ttc tcc tac atc atg gtg tgg ctg gtg act att atc gga			1393
Ile Ala Val Phe Ser Tyr Ile Met Val Trp Leu Val Thr Ile Ile Gly			
445	450		455
tac aca ctt ggg atc ccg gat gtc atc atg ggc att act ttc ctg gca			1441
Tyr Thr Leu Gly Ile Pro Asp Val Ile Met Gly Ile Thr Phe Leu Ala			
465	470		475
gca ggg aca agt gtt cca gac tgc atg gcc agc cta att gtg gcg aga			1489
Ala Gly Thr Ser Val Pro Asp Cys Met Ala Ser Leu Ile Val Ala Arg			
480	485		490
caa ggc ctt ggg gac atg gca gtc tcc aac acc ata gga agc aac gtg			1537
Gln Gly Leu Gly Asp Met Ala Val Ser Asn Thr Ile Gly Ser Asn Val			
495	500		505
ttt gac atc ctg gta gga ctt ggt gta ccg tgg ggc ctg cag acc atg			1585
Phe Asp Ile Leu Val Gly Leu Gly Val Pro Trp Gly Leu Gln Thr Met			
510	515		520
gtt gtt aat tat gga tca aca gtg aag atc aac agc cgg ggg ctg gtc			1633
Val Val Asn Tyr Gly Ser Thr Val Lys Ile Asn Ser Arg Gly Leu Val			
525	530	535	540

tat tcc gtg gtc ctg ttg ctg ggc tct gtc gct ctc acc gtc ctc ggc 1681
Tyr Ser Val Val Leu Leu Leu Gly Ser Val Ala Leu Thr Val Leu Gly
545 550 555

atc cac cta aac aag tgg cga ctg gac cgg aag ctg ggt gtc tac gtg 1729
Ile His Leu Asn Lys Trp Arg Leu Asp Arg Lys Leu Gly Val Tyr Val
560 565 570

ctg gtt ctc tac gcc atc ttc ttg tgc ttc tcc ata atg ata gag ttt 1777
Leu Val Leu Tyr Ala Ile Phe Leu Cys Phe Ser Ile Met Ile Glu Phe
575 580 585

aac gtc ttt acc ttc gtc aac ttg ccg atg tgc cgg gaa gac gat tag 1825
Asn Val Phe Thr Phe Val Asn Leu Pro Met Cys Arg Glu Asp Asp
590 595 600

cgctgagtcg cggtagctgg 1845

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<211> 603
<212> PRT
<213> Homo. sapiens

<400> 4

Met Ala Leu Arg Gly Thr Leu Arg Pro Leu Lys Val Arg Arg Arg Arg
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Glu Met Leu Pro Gln Gln Val Gly Phe Val Cys Ala Val Leu Ala Leu
20 25 30

Val Cys Cys Ala Ser Gly Leu Phe Gly Ser Leu Gly His Lys Thr Ala
35 40 45

Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg Asn Arg Lys Leu
50 55 60

Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn Cys Thr Asp Pro
65 70 75 80

Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn Lys Glu Arg Gln
85 90 95

His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu Tyr Met Phe Tyr
100 105 110

Ala Leu Ala Ile Val Cys Asp Asp Phe Phe Val Pro Ser Leu Glu Lys
115 120 125

Ile Cys Glu Arg Leu His Leu Ser Glu Asp Val Ala Gly Ala Thr Phe
130 135 140

Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala Ser Val Ile Gly
145 150 155 160

Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr Ile Val Gly Ser
165 170 175

Ala Val Phe Asn Ile Leu Cys Ile Ile Gly Val Cys Gly Leu Phe Ala
180 185 190

Gly Gln Val Val Arg Leu Thr Trp Trp Ala Val Cys Arg Asp Ser Val
195 200 205

Tyr Tyr Thr Ile Ser Val Ile Val Leu Ile Val Phe Ile Tyr Asp Glu
210 215 220

Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile Leu Tyr Val Phe
225 230 235 240

Tyr Ile Leu Ile Met Lys Tyr Asn Val Lys Met Gln Ala Phe Phe Thr
245 250 255

Val Lys Gln Lys Ser Ile Ala Asn Gly Asn Pro Val Asn Ser Glu Leu
260 265 270

Glu Ala Val Lys Glu Lys Pro Gln Tyr Gly Lys Asn Pro Val Val Met
275 280 285

Val Asp Glu Ile Met Ser Ser Ser Pro Pro Lys Phe Thr Phe Pro Glu
290 295 300

Ala Gly Leu Arg Ile Met Ile Thr Asn Lys Phe Gly Pro Arg Thr Arg
305 310 315 320

Leu Arg Met Ala Ser Arg Ile Ile Ile Asn Glu Arg Gln Arg Leu Ile
325 330 335

Asn Ser Ala Asn Gly Val Ser Ser Lys Pro Leu Gln Asn Gly Arg His
340 345 350

Glu Asn Ile Glu Asn Gly Asn Val Pro Val Glu Asn Pro Glu Asp Pro
355 360 365

Gln Gln Asn Gln Glu Gln Gln Pro Pro Pro Gln Pro Pro Pro Pro Glu
370 375 380

Pro Glu Pro Val Glu Ala Asp Phe Leu Ser Pro Phe Ser Val Pro Glu
385 390 395 400

Ala Arg Gly Asp Lys Val Lys Trp Val Phe Thr Trp Pro Leu Ile Phe
405 410 415

Leu Leu Cys Val Thr Ile Pro Asn Cys Ser Lys Pro Arg Trp Glu Lys
420 425 430

Phe Phe Met Val Thr Phe Ile Thr Ala Thr Leu Trp Ile Ala Val Phe
435 440 445

Ser Tyr Ile Met Val Trp Leu Val Thr Ile Ile Gly Tyr Thr Leu Gly
450 455 460

Ile Pro Asp Val Ile Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser
465 470 475 480

Val Pro Asp Cys Met Ala Ser Leu Ile Val Ala Arg Gln Gly Leu Gly
485 490 495

Asp Met Ala Val Ser Asn Thr Ile Gly Ser Asn Val Phe Asp Ile Leu
500 505 510

Val Gly Leu Gly Val Pro Trp Gly Leu Gln Thr Met Val Val Asn Tyr
515 520 525

Gly Ser Thr Val Lys Ile Asn Ser Arg Gly Leu Val Tyr Ser Val Val
530 535 540

Leu Leu Leu Gly Ser Val Ala Leu Thr Val Leu Gly Ile His Leu Asn
545 550 555 560

Lys Trp Arg Leu Asp Arg Lys Leu Gly Val Tyr Val Leu Val Leu Tyr
565 570 575

Ala Ile Phe Leu Cys Phe Ser Ile Met Ile Glu Phe Asn Val Phe Thr
580 585 590

Phe Val Asn Leu Pro Met Cys Arg Glu Asp Asp
595 600

<210> 5

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of artificial Sequence: an artificially synthesized primer sequence

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caggaattcc accatggcgc tccgogggac cctc

34

<210> 6

<211> 27

<212> DNA

<213> Artificial Sequence

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ccaggtaccg cgactcagcg ctaatcg

27

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: an artificially synthesized primer sequence

<400> 7

atgccttggc catagtgtgc gatg

24

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of artificial Sequence: an artificially synthesized

primer sequence

<400> 8

ctgctcacac cattggccga gttg

24

[DOCUMENT NAME] Abstract

[ABSTRACT]

[OBJECT] A novel polypeptide, a polynucleotide encoding the polypeptide, an expression vector comprising the polynucleotide, a cell transfected by the expression vector, and a method for producing the polypeptide, which are useful in screening for a substance useful in treating cell injuries due to postischemic reperfusion, are provided.

[MEANS FOR SOLUTION] The polypeptide is a potassium-dependent sodium-calcium exchanger expressed in peripheral leukocytes.

[SELECTED DRAWINGS] None